#10

FIG. 1

```
ATATTGCTGAGCTCAGGGAGTGAGGGCCCCACATTTGAGACAGTGAGCCCCAAGAAGAGG     60
GATCCCTGCTCCAGCAGCTGCAAGGTGCAAGAAGAAGAAGATCCCAGGGAGGAAAATGTG    120
                                                         M  C     2
CTGGAGACCCCTGTGTCGGTTCCTGTGGCTTTGGTCCTATCTGTCTTATGTTCAAGCAGT    180
 W  R  P  L  C  R  F  L  W  L  W  S  Y  L  S  Y  V  Q  A  V      22
GCCTATCCAGAAAGTCCAGGATGACACCAAAACCCTCATCAAGACCATTGTCACCAGGAT    240
 P  I  Q  K  V  Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I      42
CAATGACATTTCACACACGCAGTCGGTATCCGCCAAGCAGAGGGTCACTGGCTTGGACTT    300
 N  D  I  S  H  T  Q  S  V  S  A  K  Q  R  V  T  G  L  D  F      62
CATTCCTGGGCTTCACCCCATTCTGAGTTTGTCCAAGATGGACCAGACTCTGGCAGTCTA    360
 I  P  G  L  H  P  I  L  S  L  S  K  M  D  Q  T  L  A  V  Y      82
TCAACAGGTCCTCACCAGCCTGCCTTCCCAAAATGTGCTGCAGATAGCCAATGACCTGGA    420
 Q  Q  V  L  T  S  L  P  S  Q  N  V  L  Q  I  A  N  D  L  E     102
GAATCTCCGAGACCTCCTCCATCTGCTGGCCTTCTCCAAGAGCTGCTCCCTGCCTCAGAC    480
 N  L  R  D  L  L  H  L  L  A  F  S  K  S  C  S  L  P  Q  T     122
CAGTGGCCTGCAGAAGCCAGAGAGCCTGGATGGCGTCCTGGAAGCCTCACTCTACTCCAC    540
 S  G  L  Q  K  P  E  S  L  D  G  V  L  E  A  S  L  Y  S  T     142
AGAGGTGGTGGCTTTGAGCAGGCTGCAGGGCTCTCTGCAGGACATTCTTCAACAGTTGGA    600
 E  V  V  A  L  S  R  L  Q  G  S  L  Q  D  I  L  Q  Q  L  D     162
TGTTAGCCCTGAATGCTGAAGTTTCAAAGGCCACCAGGCTCCCAAGAATCATGTAGAGGG    660
 V  S  P  E  C  *                                               167
AAGAAACCTTGGCTTCCAGGGGTCTTCAGGAGAAGAGAGCCATGTGCACACATCCATCAT    720
TCATTTCTCTCCCTCCTGTAGACCACCCATCCAAAGGCATGACTCCACAATGCTTGACTC    780
AAGTTATCCACACAACTTCATGAGCACAAGGAGGGGCCAGCCTGCAGAGGGGACTCTCAC    840
CTAGTTCTTCAGCAAGTAGAGATAAGAGCCATCCCATCCCCTCCATGTCCCACCTGCTCC    900
GGGTACATGTTCCTCCGTGGGTACACGCTTCGCTGCGGCCCAGGAGAGGTGAGGTAGGGA    960
TGGGTAGAGCCTTTGGGCTGTCTCAGAGTCTTTGGGAGCACCGTGAAGGCTGCATCCACA   1020
CACAGCTGGAAACTCCCAAGCAGCACACGATGGAAGCACTTATTTATTTATTCTGCATTC   1080
TATTTTGGATGGATCTGAAGCAAGGCATCAGCTTTTTCAGGCTTTGGGGGTCAGCCAGGA   1140
TGAGGAAGGCTCCTGGGGTGCTGCTTTCAATCCTATTGATGGGTCTGCCCGAGGCAAACC   1200
TAATTTTTGAGTGACTGGAAGGAAGGTTGGGATCTTCCAAACAAGAGTCTATGCAGGTAG   1260
CGCTCAAGATTGACCTCTGGTGACTGGTTTGTTTCTATTGTGACTGACTCTATCCAAAC   1320
ACGTTTGCAGCGGCATTGCCGGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTT   1380
TGTCAAGTGTAATATGTATCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGT   1440
GAAGGATCCGGAAGTGTTCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGA   1500
GGCATTTTCTTACCTCTGTGGCCACATAGTGTGGCTTTGTGAAAAGGACAAAGGAGTTGA   1560
CTCTTTCCGGAACATTTGGAGTGTACCAGGCACCCTTGGAGGGGCTAAAGCTACAGGCCT   1620
TTTGTTGGCATATTGCTGAGCTCAGGGAGTGAGGGCCCCACATTTGAGACAGTGAGCCCC   1680
AAGAAAAGGGTCCCTGGTGTAGATCTCCAAGGTTGTCCAGGGTTGATCTCACAATGCGTT   1740
TCTTAAGCAGGTAGACGTTTGCATGCCAATATGTGGTTCTCATCTGATTGGTTCATCCAA   1800
AGTAGAACCCTGTCTCCCACCCATTCTGTGGGGAGTTTTGTTCCAGTGGGAATGAGAAAT   1860
CACTTAGCAGATGGTCCTGAGCCCTGGGCCAGCACTGCTGAGGAAGTGCCAGGGCCCCAG   1920
GCCAGGCTGCCAGAATTGCCCTTCGGGCTGGAGGATGAACAAAGGGGCTTGGGTTTTTCC   1980
ATCACCCCTGCACCCTATGTCACCATCAAACTGGGGGGCAGATCAGTGAGAGGACACTTG   2040
ATGGAAAGCAATACACTTTAAGACTGAGCACAGTTTCGTGCTCAGCTCTGTCTGGTGCTG   2100
TGAGCTAGAGAAGCTCACCACATACATATAAAAATCAGAGGCTCATGTCCCTGTGGTTAG   2160
ACCCTACTCGCGGCGGTGTACTCCACCACAGCAGCACCGCACCGCTGGAAGTACAGTGCT   2220
GTCTTCAACAGGTGTGAAAGAACCTGAGCTGAGGGTGACAGTGCCCAGGGGAACCCTGCT   2280
TGCAGTCTATTGCATTTACATACCGCATTTCAGGGCACATTAGCATCCACTCCTATGGTA   2340
GCACACTGTTGACAATAGGACAAGGGATAGGGGTTGACTATCCCTTATCCAAAATGCTTG   2400
GGACTAGAAGAGTTTTGGATTTTAGAGTCTTTTCAGGCATAGGTATATTTGAGTATATAT   2460
AAAATGAGATATCTTGGGGATGGGGCCCAAGTATAAACATGAAGTTCATTTATATTTCAT   2520
AATACCGTATAGACACTGCTTGAAGTGTAGTTTTATACAGTGTTTTAAATAACGTTGTAT   2580
GCATGAAAGACGTTTTTACAGCATGAACCTGTCTACTCATGCCAGCACTCAAAAACCTTG   2640
GGGTTTTGGAGCAGTTTGGATCTTGGGTTTTCTGTTAAGAGATGGTTAGCTTATACCTAA   2700
AACCATAATGGCAAACAGGCTGCAGGACCAGACTGGATCCTCAGCCCTGAAGTGTGCCCT   2760
TCCAGCCAGGTCATACCCTGTGGAGGTGAGCGGGATCAGGTTTTGTGGTGCTAAGAGAGG   2820
AGTTGGAGGTAGATTTTGGAGGATCTGAGGGC                               2852
```

FIG.2

```
---G--GTTG CAAGGCCCAA GAAGCCCA-- -TCCTGGGAA GGAAAATGCA    50
TTGGGGAACC CTGTG-CGGA TTCTTGTGGC TTTGGCCCTA TCTTTTCTAT   100
GTCCAAGCTG TGCCCATCCA AAAAGTCCAA GATGACACCA AAACCCTCAT   150
CAAGACAATT GTCACCAGGA TCAATGACAT TTCACACACG CAGTCAGTCT   200
CCTCCAAACA GAAAGTCACC GGTTTGGACT TCATTCCTGG GCTCCACCCC   250
ATCCTGACCT TATCCAAGAT GGACCAGACA CTGGCAGTCT ACCAACAGAT   300
CCTCACCAGT ATGCCTTCCA GAAACGTGAT CCAAATATCC AACGACCTGG   350
AGAACCTCCG GGATCTTCTT CACGTGCTGG CCTTCTCTAA GAGCTGCCAC   400
TTGCCCTGGG CCAGTGGCCT GGAGACCTTG GACAGCCTGG GGGGTGTCCT   450
GGAAGCTTCA GGCTACTCCA CAGAGGTGGT GGCCCTGAGC AGGCTGCAGG   500
GGTCTCTGCA GGACATGCTG TGGCAGCTGG ACCTCAGCCC TGGGTGCTGA   550
GGCCTTGAAG GTCACTCTTC CTGCAAGGAC T-ACGTTAAG GGAAGGAACT   600
CTGGTTTCCA GGTATCTCCA GGATTGAAGA GCATTGCATG GACACCCCTT   650
ATCCAGGACT CTGTCAATTT CCCTGACTCC TCTAAGCCAC TCTTCCAAAG   700
G                                                        701
```

1	MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
16	LEU PHE TYR VAL GLN ALA↓VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR GLN SER VAL SER SER LYS GLN LYS VAL THR GLY LEU
61	ASP PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET
76	ASP GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO
91	SER ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG
106	ASP LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO
121	TRP ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU
136	GLU ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU
151	GLN GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO
166	GLY CYS END

FIG.3

```
MOUSE   MCWRPLCRFL WLWSYLSYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS   50
         * **  *      *  *
HUMAN   MHWGTLCGFL WLWPYLFYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS

MOUSE   VSAKQRVTGL DFIPGLHPIL SLSKMDQTLA VYQQVLTSLP SQNVLQIAND  100
          *                   -               -   -   *     *
HUMAN   VSSKQKVTGL DFIPGLHPIL TLSKMDQTLA VYQQILTSMP SRNVIQISND

MOUSE   LENLRDLLHL LAFSKSCSLP QTSGLQKPES LDGVLEASLY STEVVALSRL  150
                 -        *   **   ***-   *      *
HUMAN   LENLRDLLHV LAFSKSCHLP WASGLETLDS LGGVLEASGY STEVVALSRL

MOUSE   QGSLQDILQQ LDVSPEC                                      167
              - *    -  *
HUMAN   QGSLQDMLWQ LDLSPGC
```

FIG.4

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

1	Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr
16	Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp
61	Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp
76	Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser
91	Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp
106	Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro Gln
121	Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu Glu
136	Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln
151	Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro Glu
166	Cys End

FIG.5

1	MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
16	LEU PHE TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR SER VAL SER SER LYS GLN LYS VAL THR GLY LEU ASP
61	PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET ASP
76	GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO SER
91	ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG ASP
106	LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO TRP
121	ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU GLU
136	ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU GLN
151	GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO GLY
166	CYS END

FIG.6

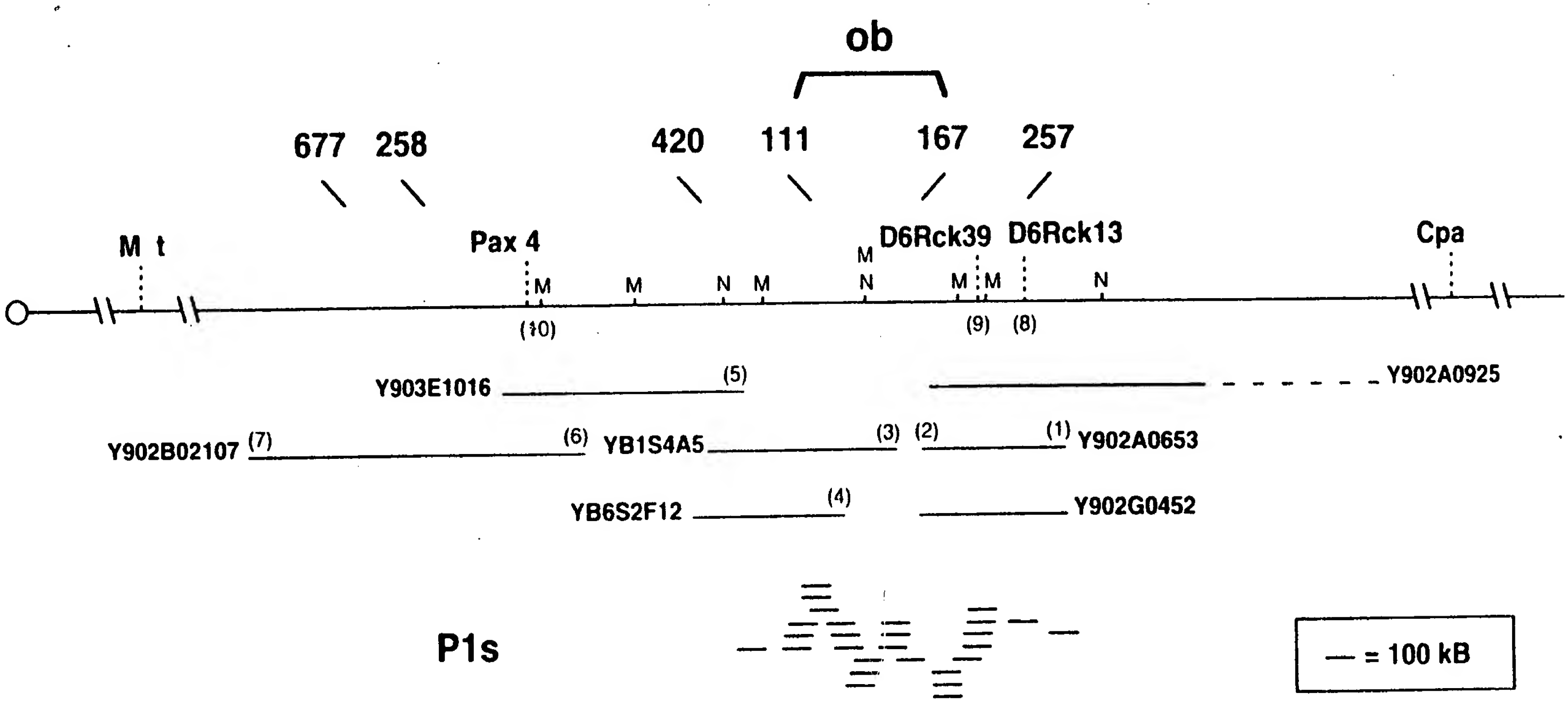

ob
677
258
420
111
167
257
M t
Pax 4
D6Rck39
D6Rck13
Cpa
M
N
(10)
(9)
(8)
Y903E1016
(5)
Y902A0925
Y902B02107
(7)
(6)
YB1S4A5
(3)
(2)
(1)
Y902A0653
YB6S2F12
(4)
Y902G0452
P1s
— = 100 kB

FIG.7

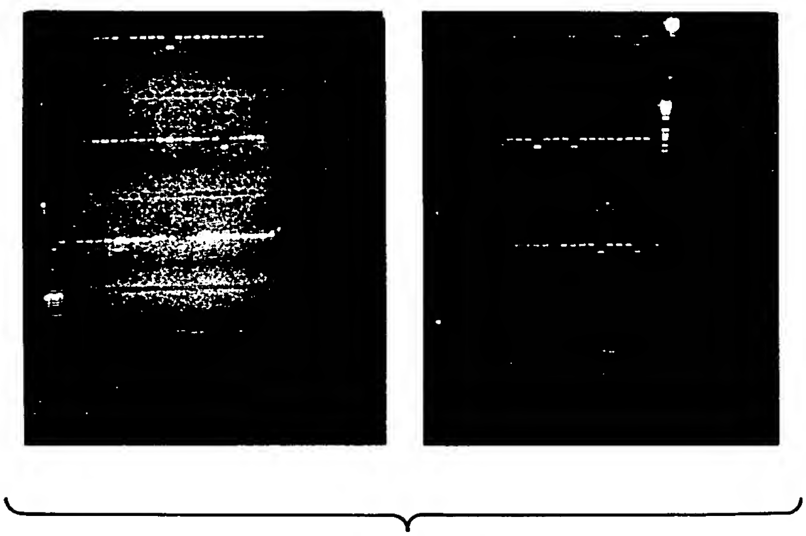


FIG.8

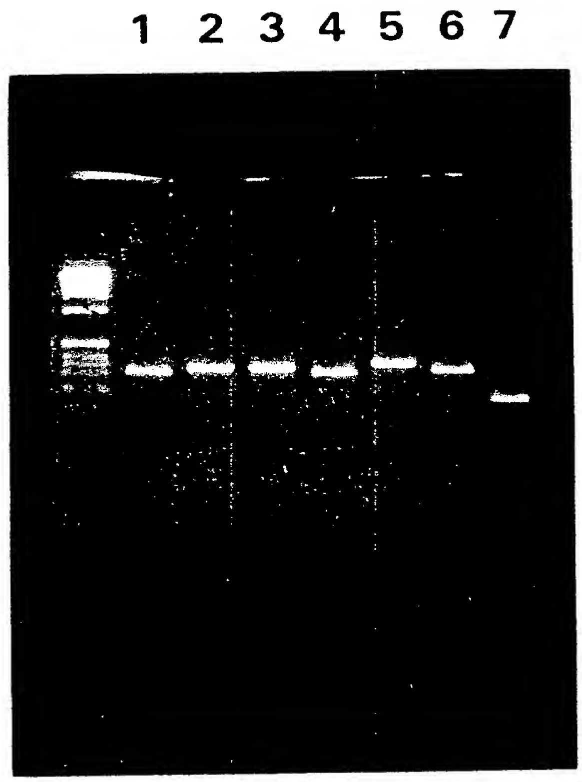


FIG.9

```
           +10        +20        +30        +40
GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG
---------- ---------- ---------- ---------- ----------
CACGTTCTTC TTCTTCTAGG GTCCCGTCCT TTTACACGAC CTCTGGGGAC

           +10        +20        +30        +40
TGTCGGGTCC NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC
---------- ?----?---- ---------- --------?- ----------
ACAGCCCAGG NCACCNAAAC CAGGATAGAC AGAATACANG TTCGTCACGG

           +10        +20        +30        +40
TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA
---------- ---------- ---------- ---------- ----------
ATAGGTCTTT CAGGTCCTAC TGTGGTTTTC GGAGTAGTTC TGGTAACAGT

           +10        +20        +30        +40
NCAGGATCAC TGANATTTCA CACACG
?--------- ---?------ ------
NGTCCTAGTG ACTNTAAAGT GTGTGC
```

FIG.10

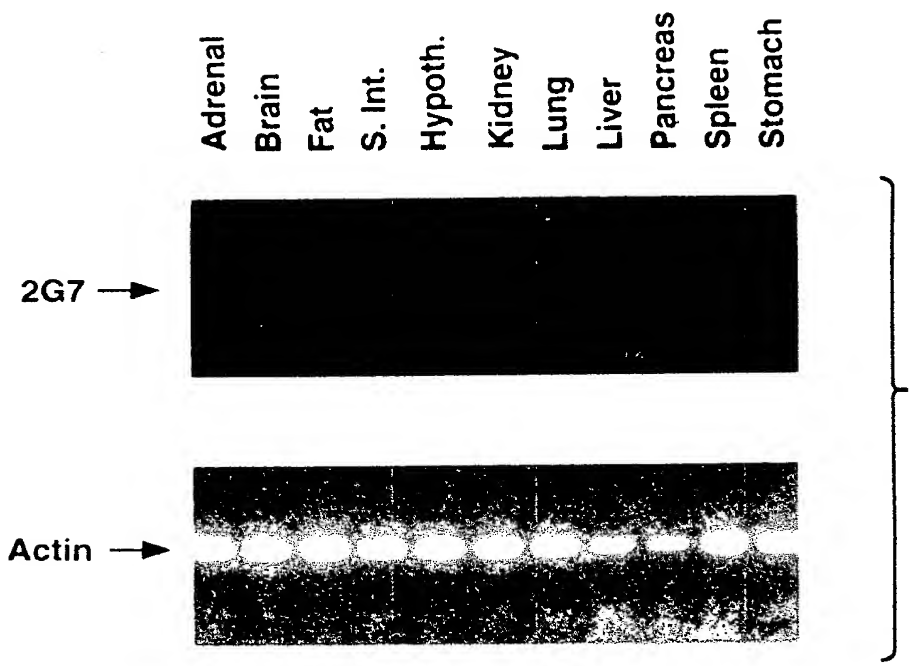

Adrenal
Brain
Fat
S. Int.
Hypoth.
Kidney
Lung
Liver
Pancreas
Spleen
Stomach
2G7
Actin

FIG.11A

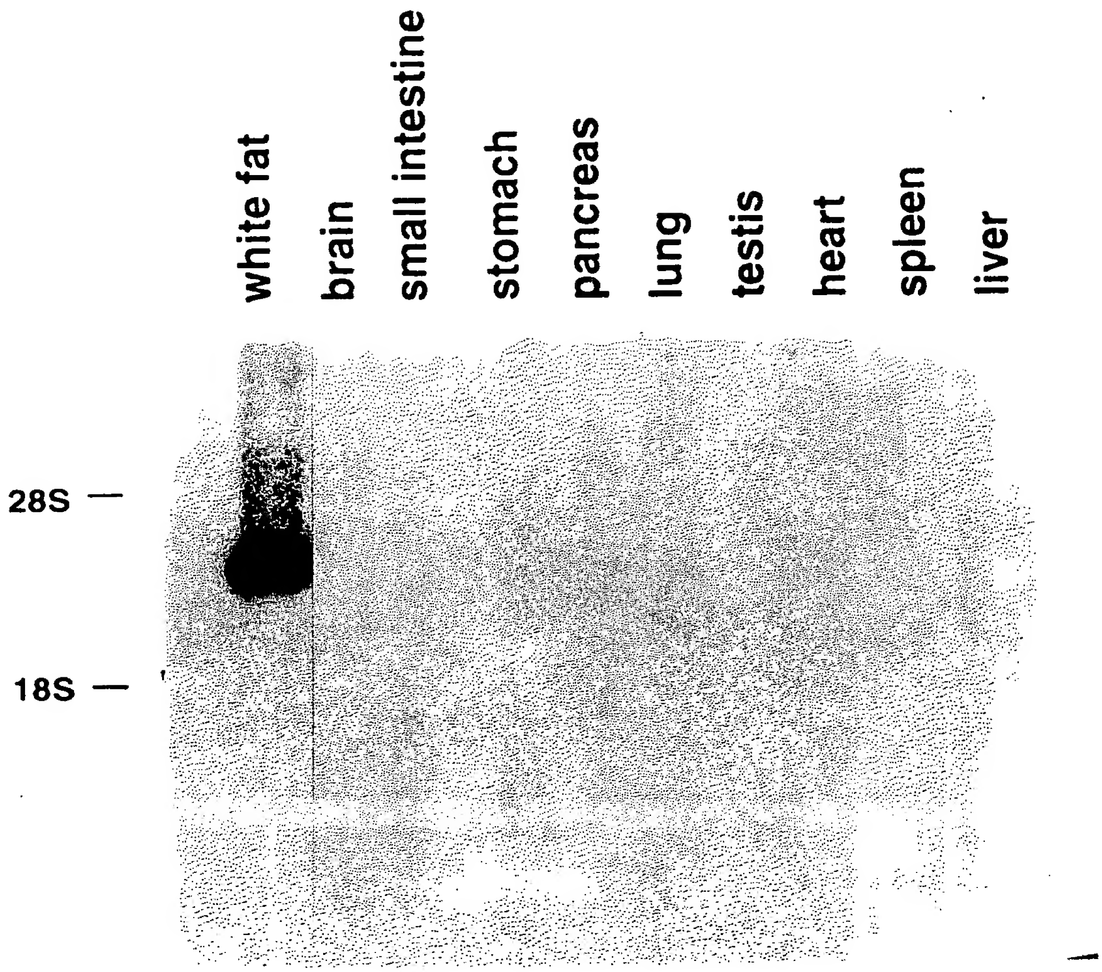

white fat
brain
small intestine
stomach
pancreas
lung
testis
heart
spleen
liver
28S
18S

FIG.11B


C57BL/6J +/+
C57BL/6J ob/ob
SM/Ckc-+Dac-+/+
SM/Ckc-+Dac-ob2J/ob2J
1kB
Actin
2G7
1
2
3
4
5

FIG.12A

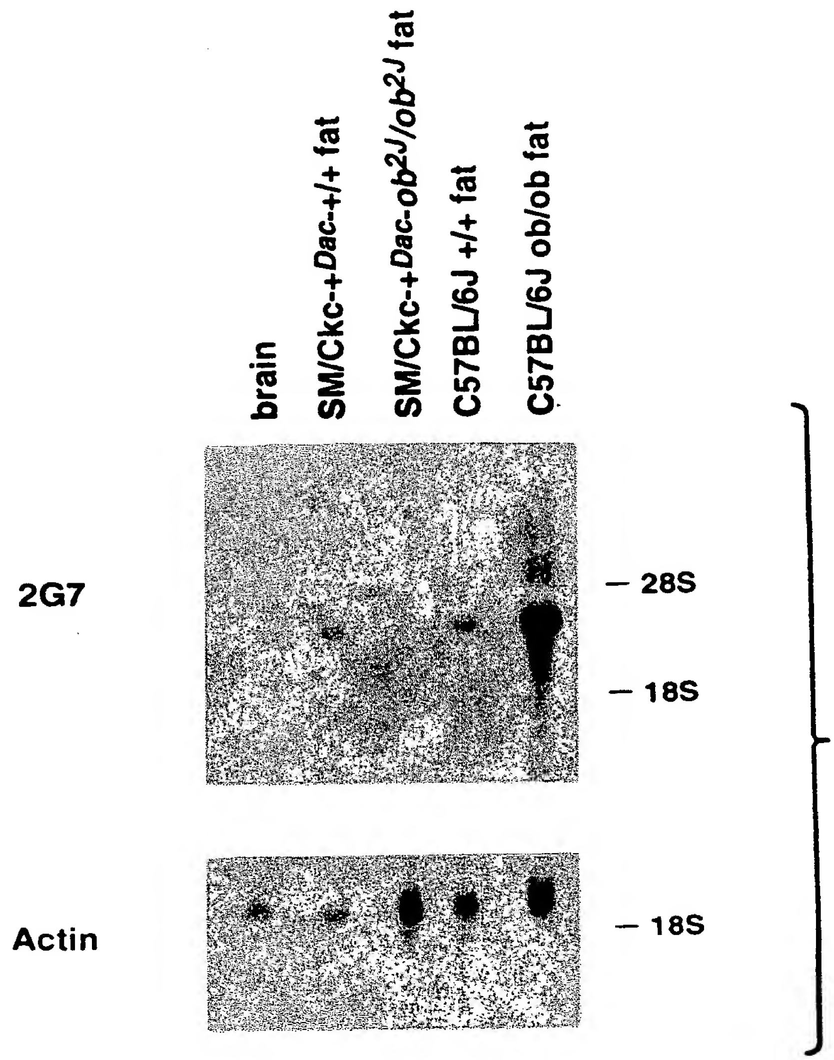

brain
SM/Ckc-+Dac-+/+ fat
SM/Ckc-+Dac-ob2J/ob2J fat
C57BL/6J +/+ fat
C57BL/6J ob/ob fat
2G7
— 28S
— 18S
Actin
— 18S

FIG.12B

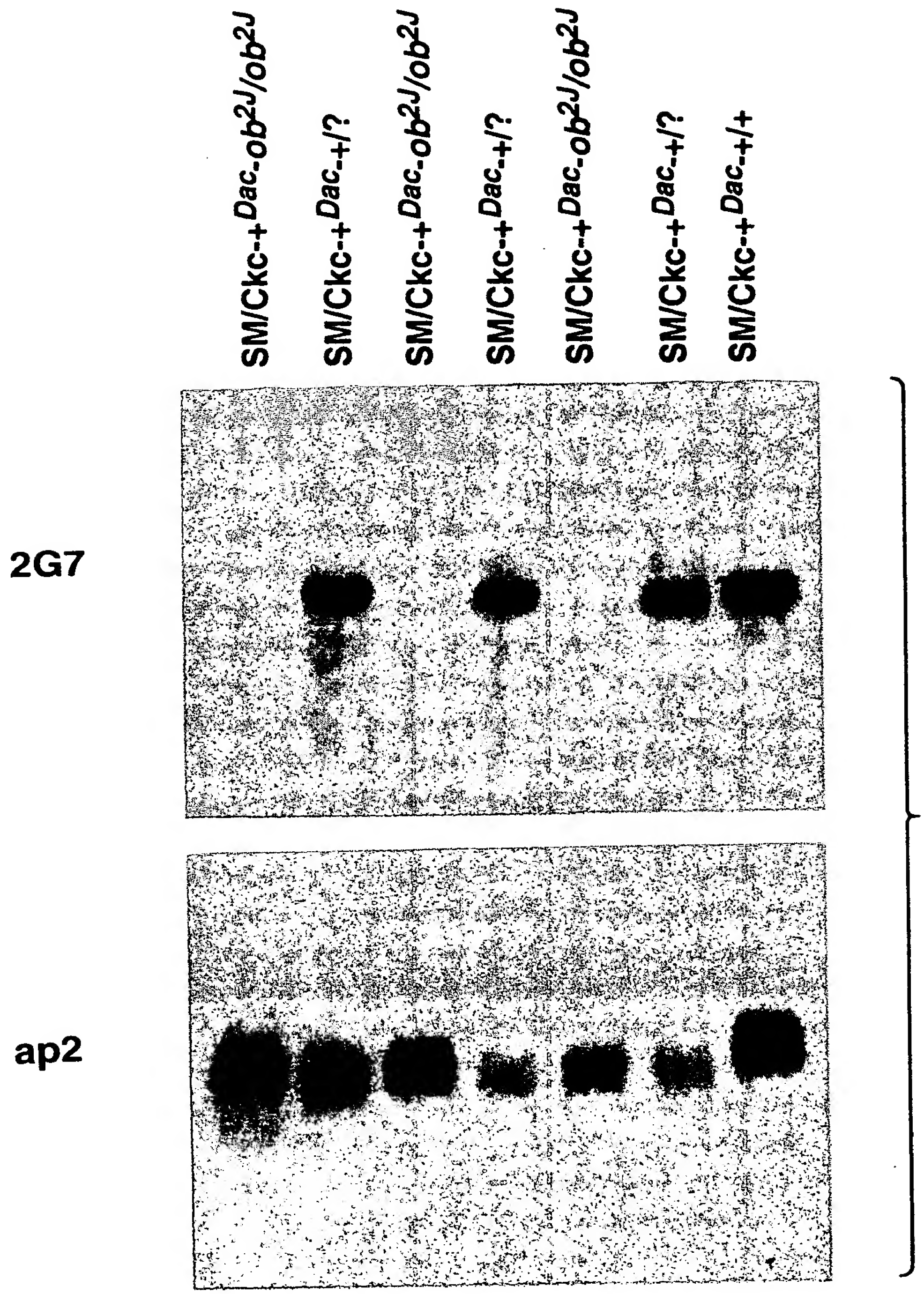

SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/?
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/?
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/?
SM/Ckc-+Dac-+/+
2G7
ap2

FIG.13

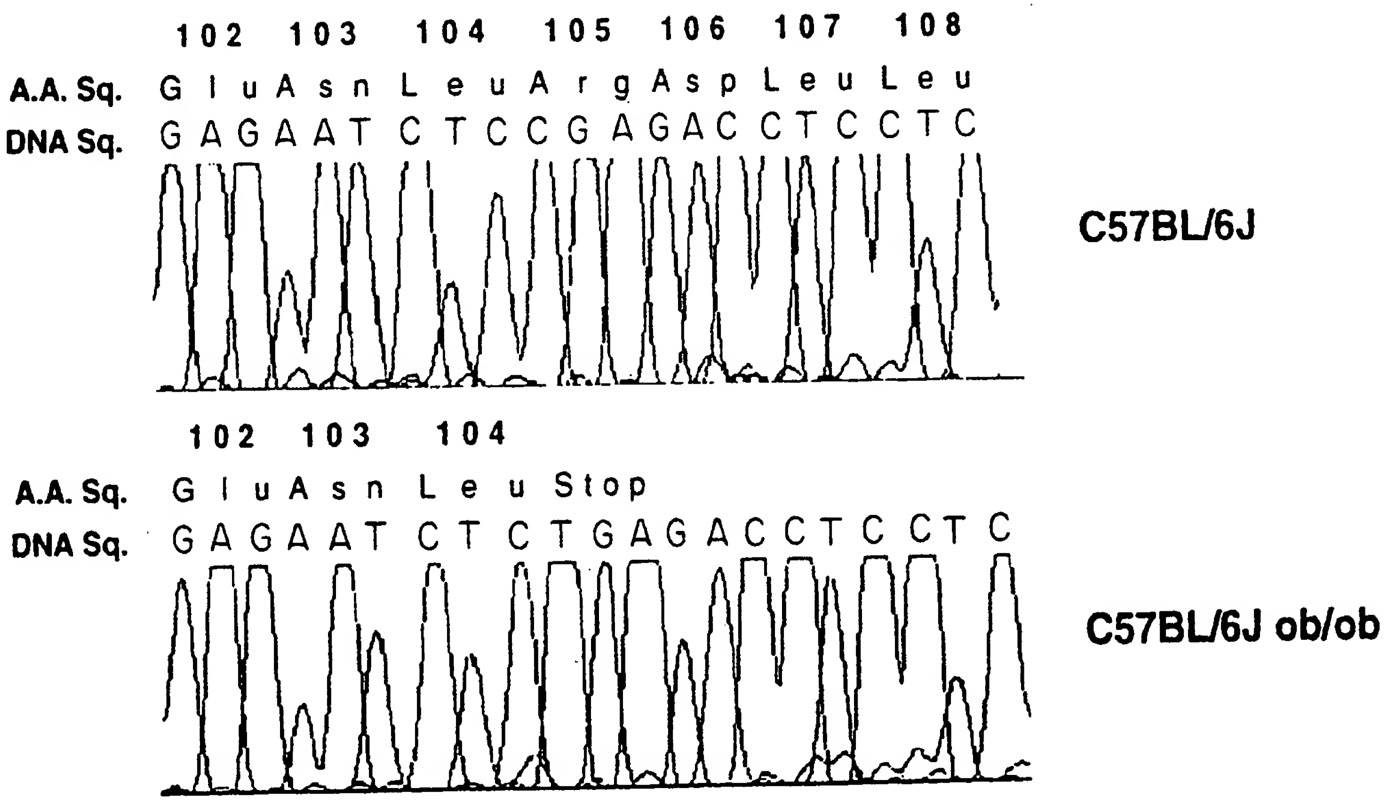

102 103 104 105 106 107 108
A.A. Sq. G l u A s n L e u A r g A s p L e u L e u
DNA Sq. G A G A A T C T C C G A G A C C T C C T C
C57BL/6J
102 103 104
A.A. Sq. G l u A s n L e u Stop
DNA Sq. G A G A A T C T C T G A G A C C T C C T C
C57BL/6J ob/ob

FIG.14

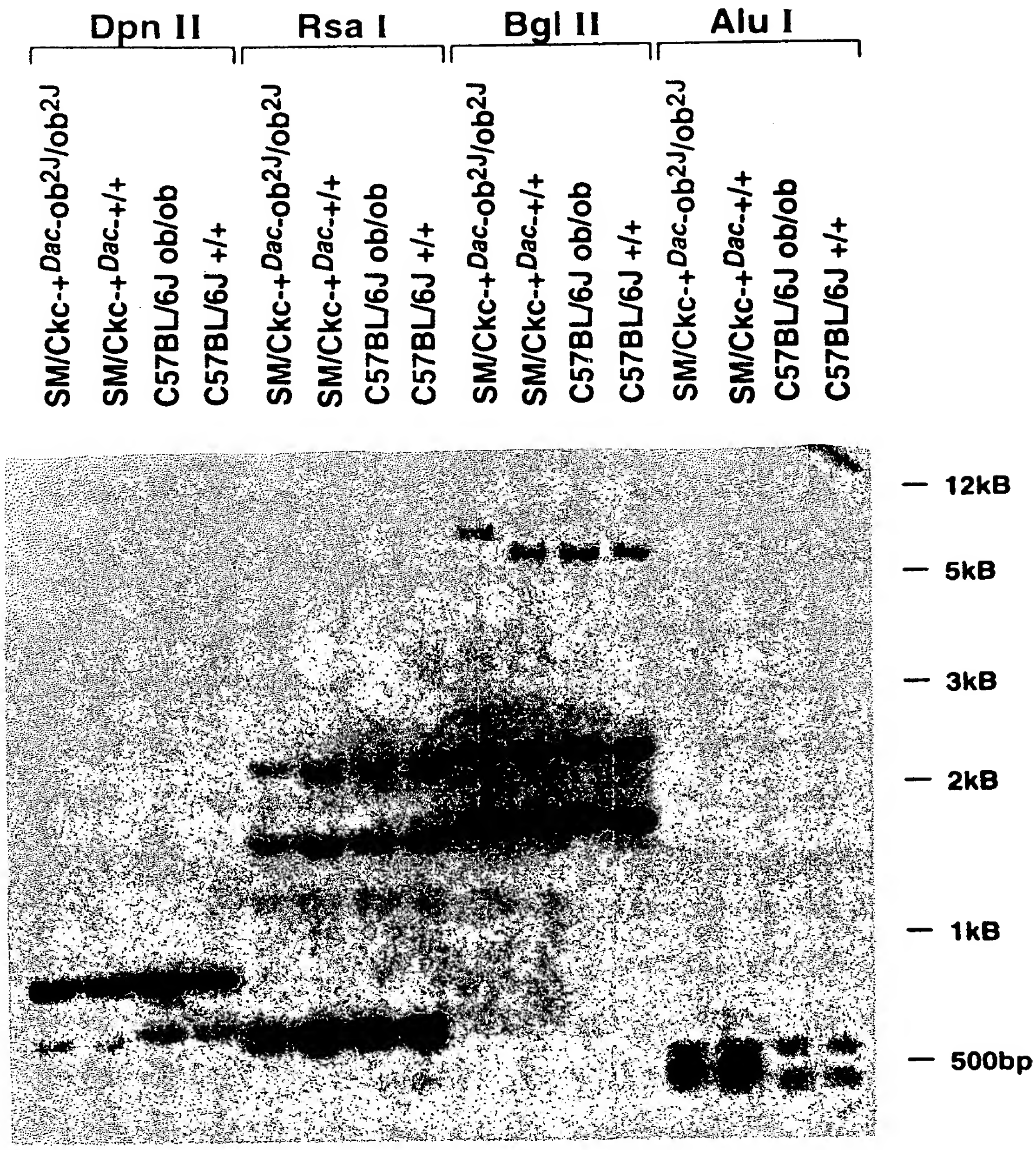

Dpn II
Rsa I
Bgl II
Alu I
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
12kB
5kB
3kB
2kB
1kB
500bp

FIG. 15A

BglII Digests

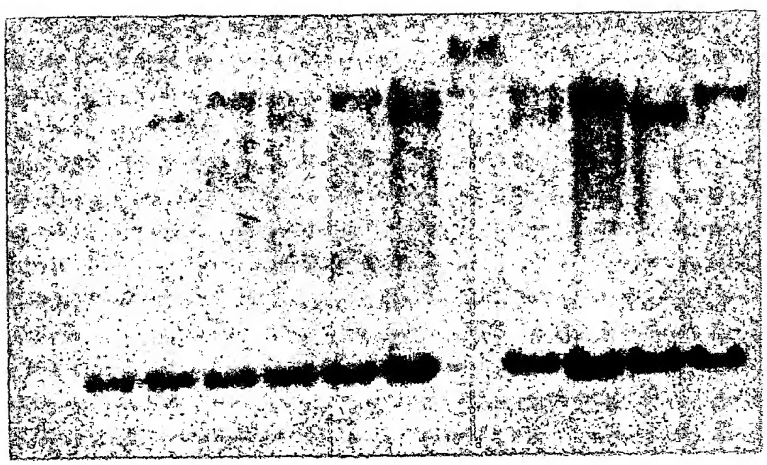


FIG.15B

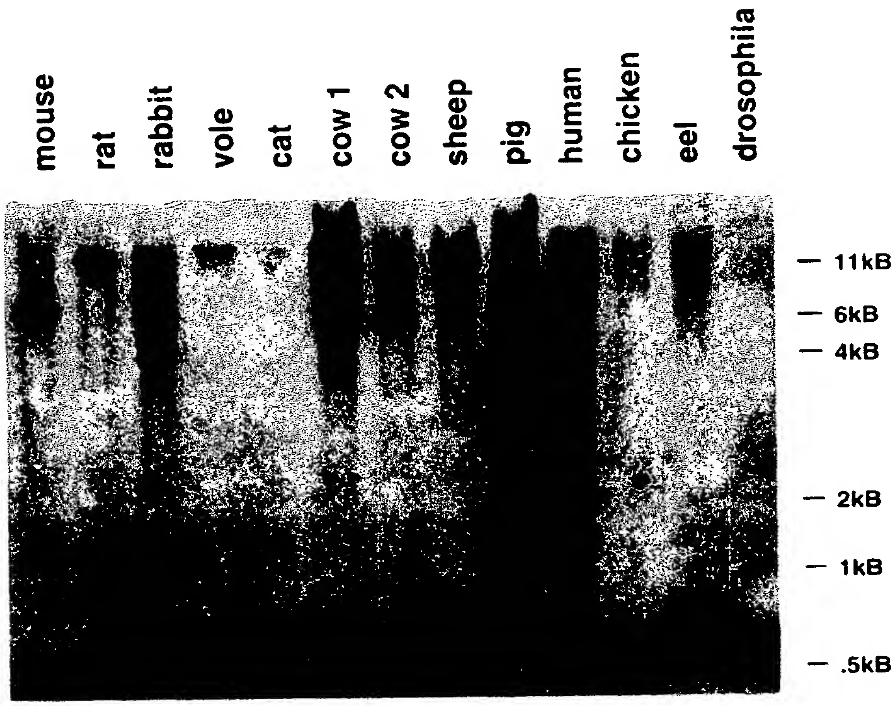

mouse
rat
rabbit
vole
cat
cow 1
cow 2
sheep
pig
human
chicken
eel
drosophila
11kB
6kB
4kB
2kB
1kB
.5kB

FIG.16

T7 PROMOTER PRIMER 69348-1
------------------->
T7 PROMOTER
--------------->

BGLII | LAC OPERATOR | XBAI

AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTACA

RBS | NCOI | HIS•TAG

AATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGC
MetGlySerSerHisHisHisHisHisHisSerSerGly

NDEI | XHOI | BAMHI

CTGGTGCCGCGCGGCAGCCATATGCTCGAGGATCCCGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCT
LeuValProArgGlySerHisMetLeuGluAspProAlaAlaAsnLysAlaArgLysGluAlaGluLeuAla
THROMBIN

BPUI1021 | T7 TERMINATOR

GCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
AlaAlaThrAlaGluGlnEnd
<-----------------------
T7 TERMINATOR PRIMER #69337-1

FIG.17

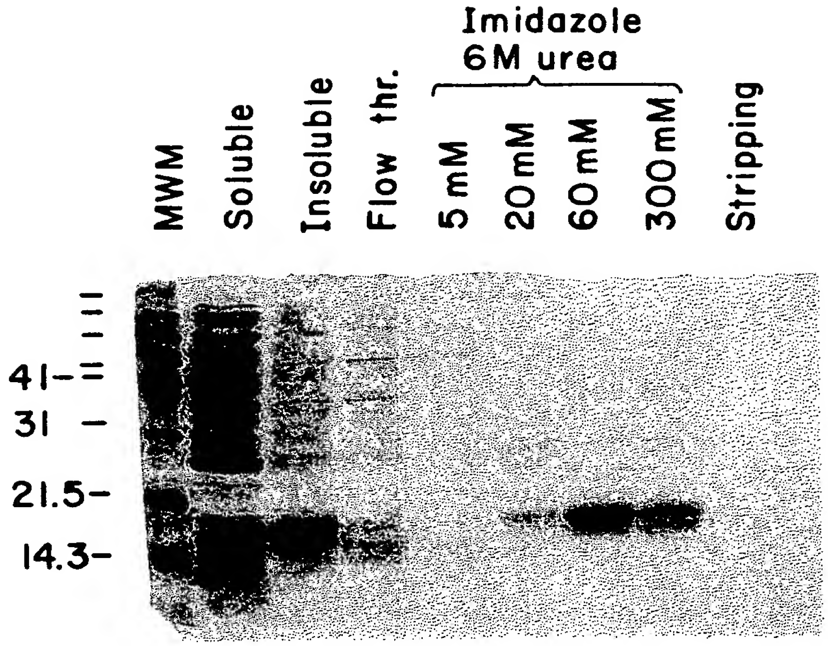


FIG.18A

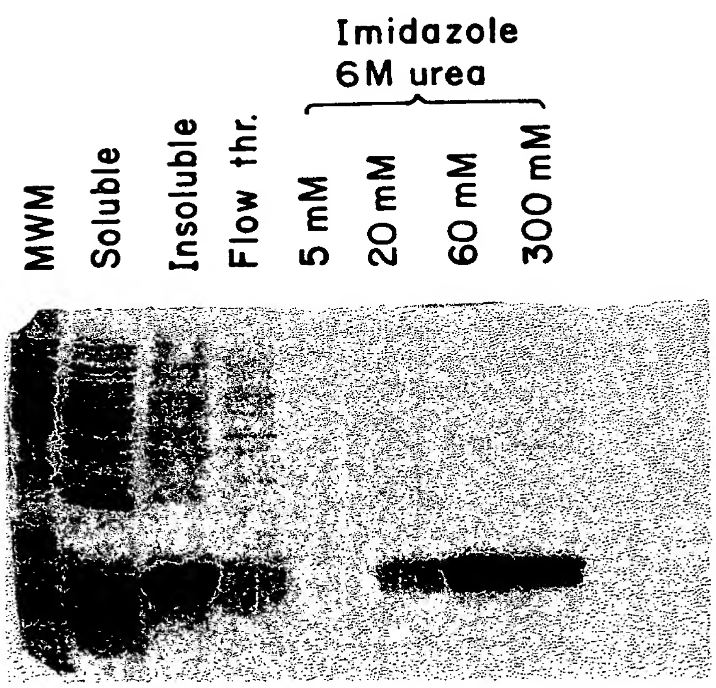


FIG.18B

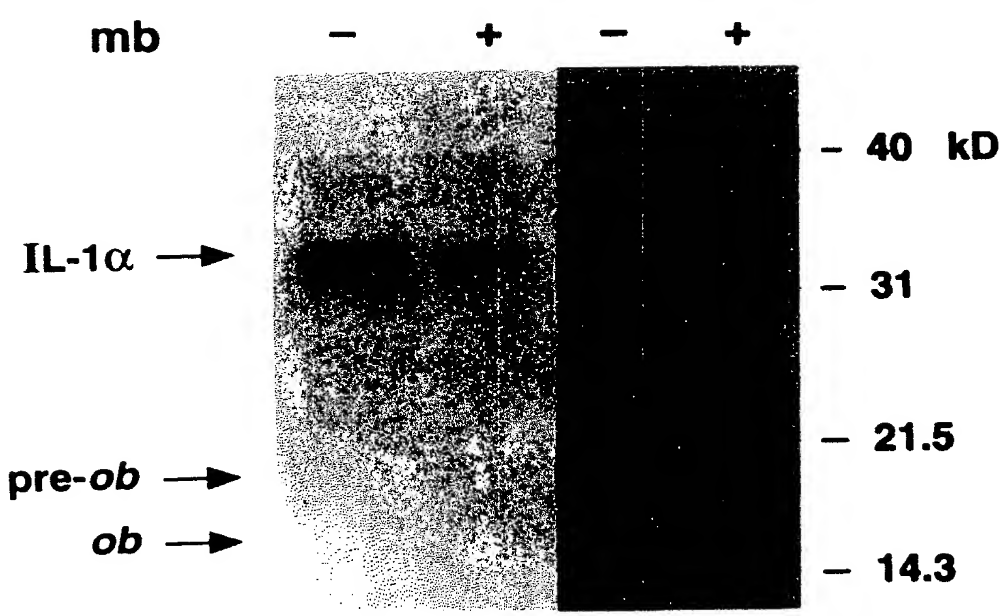


FIG.19A

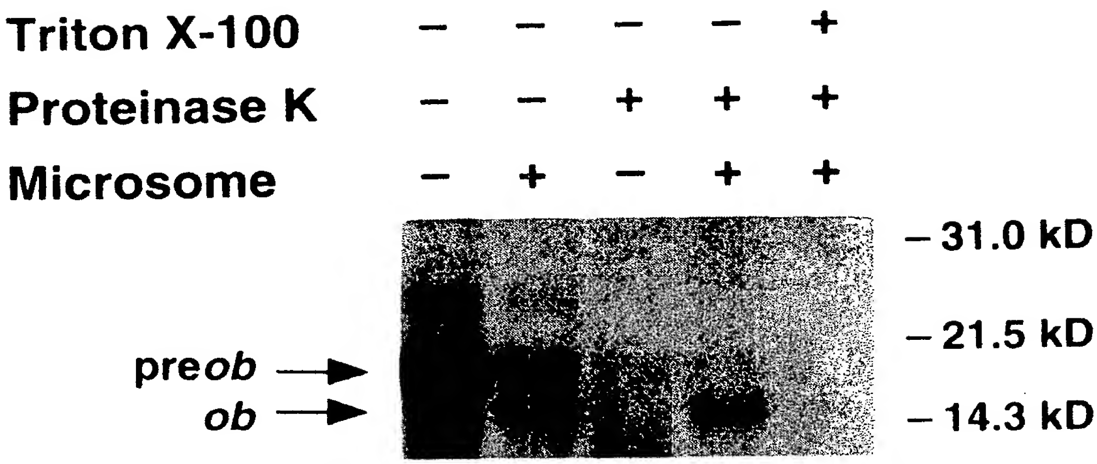

Triton X-100 – – – – +
Proteinase K – – + + +
Microsome – + – + +
preob
ob
– 31.0 kD
– 21.5 kD
– 14.3 kD

FIG.19B

```
         10         20         30         40         50
GGTTGCAAGG CCCAAGAAGC CCATCCTGGG AAGGAAAATG CATTGGGGAA
             HOB 1G F                   START

         60         70         80         90        100
CCCTGTGCGG ATTCTTGTGG CTTTGGCCCT ATCTTTTCTA TGTCCAAGCT

        110        120        130        140        150
GTGCCCATCC AAAAAGTCCA AGATGACACC AAAACCCTCA TCAAGACAAT

                                  5' OF 1ST INTRON
        160        170        180        190        200
TGTCACCAGG ATCAATGACA TTTCACACAC GGTAAGGAGA GTATGCGGGG

        210        220        230        240        250
ACAAAGTAGA ACTGCAGCCA GCCCAGCACT GGCTCCTAGT GGCACTGGAC
                                             HOB 1G R
```

FIG.20A

```
       260        270        280        290        300
CCAGATAGTC CAAGAAACAT TTATTGAACG CCTCCTGAAT GCCAGGCACC

       310        320        330        340        350
TACTGGAAGC TGAGAAGGAT TTTGGATAGC ACAGGGCTCC ACTCTTTCTG

       360        370        380        390        400
GTTGTTTCTT NTGGCCCCCT CTGCCTGCTG AGATNCCAGG GGTTAGNGGT

       410        420        430        440        450
TCTTAATTCC TAAA------ ---------- ---------- --------CT
                      GAP OF SEQUENCE (~1.4 KB)

       460        470        480        490        500
GGTTCTTTCA GGAAGAGGCC ATGTAAGAGA AAGGAATTGA CCTAGGGAAA
```

FIG.20A-1

```
     510        520        530        540        550
ATTGGCCTGG GAAGTGGAGG GAACGGATGG TGTGGGAAAA GCAGGAATCT

     560        570        580        590        600
CGGAGACCAG CTTAGAGGCT TGGCAGTCAC CTGGGTGCAG GANACAAGGG

     610        620        630        640        650
CCTGAGCCAA AGTGGTGAGG GAGGGTGGAA GGAGACAGCC CAGAGAATGA

     660        670        680        690        700
CCCTCCATGC CCACGGGGAA GGCAGAGGGC TCTGAGAGCG ATTCCTCCCA
                      3' OF 1ST INTRON

     710        720        730        740        750
CATGCTGAGC ACTTGTTCTC CCTCTTCCTC CTNCATAGCA GTCAGTCTCC
 HOB 2G F
```

FIG.20A-2

```
        760        770        780        790        800
TCCAAACAGA AAGTCACCGG TTTGGACTTC ATTCCTGGGC TCCACCCCAT
        810        820        830        840        850
CCTGACCTTA TCCAAGATGG ACCAGACACT GGCAGTCTAC CAACAGATCC
        860        870        880        890        900
TCACCAGTAT GCCTTCCAGA AACGTGATCC AAATATCCAA CGACCTGGAG
        910        920        930        940        950
AACCTCCGGG ATCTTCTTCA CGTGCTGGCC TTCTCTAAGA GCTGCCACTT
        960        970        980        990       1000
GCCCTGGGCC AGTGGCCTGG AGACCTTGGA CAGCCTGGGG GGTGTCCTGG
```

FIG.20A-3

```
      1010       1020       1030       1040       1050
AAGCTTCAGG CTACTCCACA GAGGTGGTGG CCCTGAGCAG GCTGCAGGGG

      1060       1070       1080       1090       1100
TCTCTGCAGG ACATGCTGTG GCAGCTGGAC CTCAGCCCTG GGTGCTGAGG
                                                  STOP

      1110       1120       1130       1140       1150
CCTTGAAGGT CACTCTTCCT GCAAGGACTA CGTTAAGGGA AGGAACTCTG

      1160       1170       1180       1190       1200
GCTTTCCAGG TATCTCCAGG ATTGAAGAGC ATTGCATGGA CACCCCTTAT
            HOB 2G R

      1210       1220       1230       1240       1249
CCAGGACTCT GTCAATTTCC CTGACTCCTC TAAGCCACTC TTCCAAAGG
```

FIG. 20A-4

MOUSE OB STRUCTURE

```
!st ex   1st intr      2nd ex        2nd intr      3rd exon

_______///////////_____ATG_________/////////////_____________TGA_____
                       start                                 stop
```

FIG.20B

HUMAN OB STRUCTURE

```
                    1st exon        1st intr        2nd exon

..................___ATG__________////////////__________________TGA____
                     start                                      stop
```

FIG.20C

FIG.21A

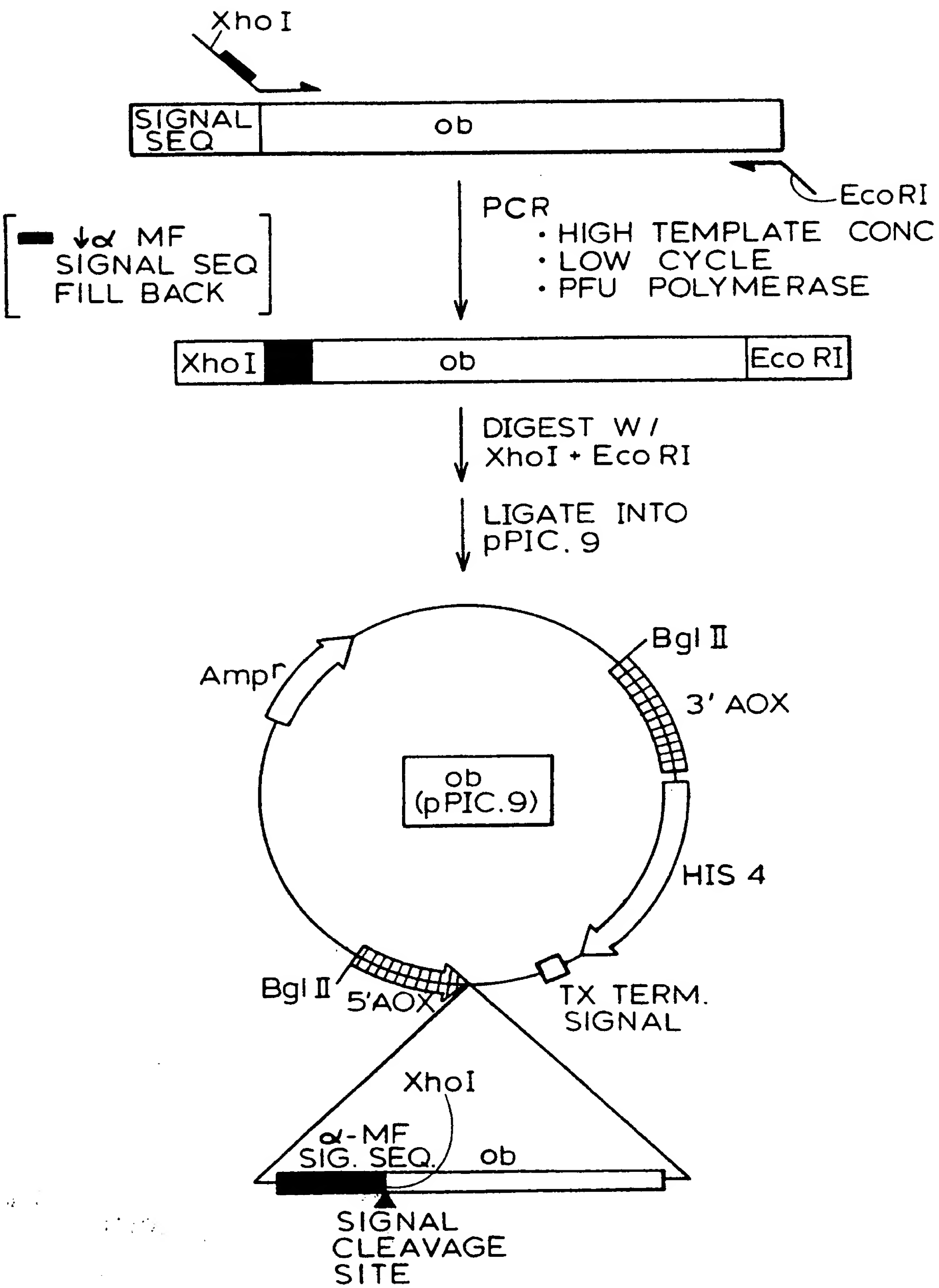

XhoI
SIGNAL SEQ
ob
EcoRI
PCR
• HIGH TEMPLATE CONC.
• LOW CYCLE
• PFU POLYMERASE
↓α MF
SIGNAL SEQ
FILL BACK
XhoI
ob
Eco RI
DIGEST W/
XhoI + Eco RI
LIGATE INTO
pPIC.9
Amp^r
Bgl II
3' AOX
ob
(pPIC.9)
HIS 4
Bgl II
5'AOX
TX TERM.
SIGNAL
XhoI
α-MF
SIG. SEQ.
ob
SIGNAL
CLEAVAGE
SITE

FIG.21B

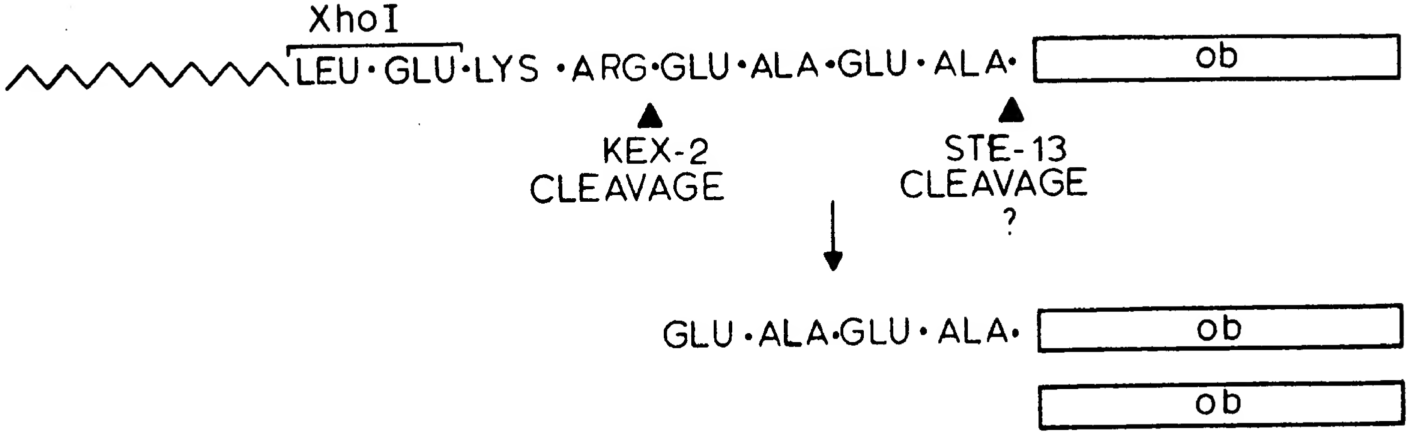


FIG.21C

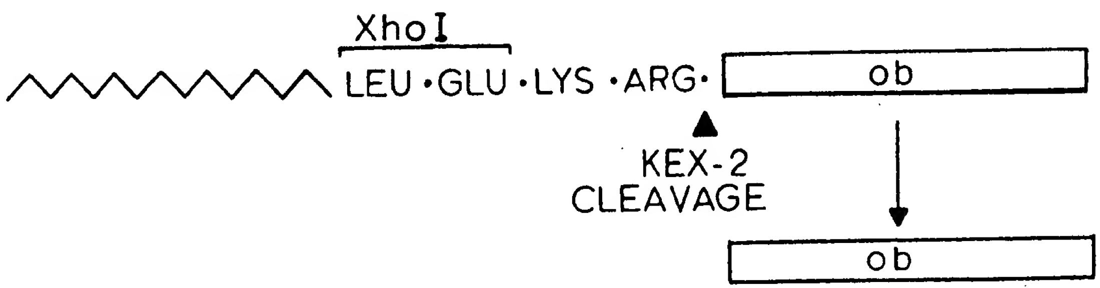
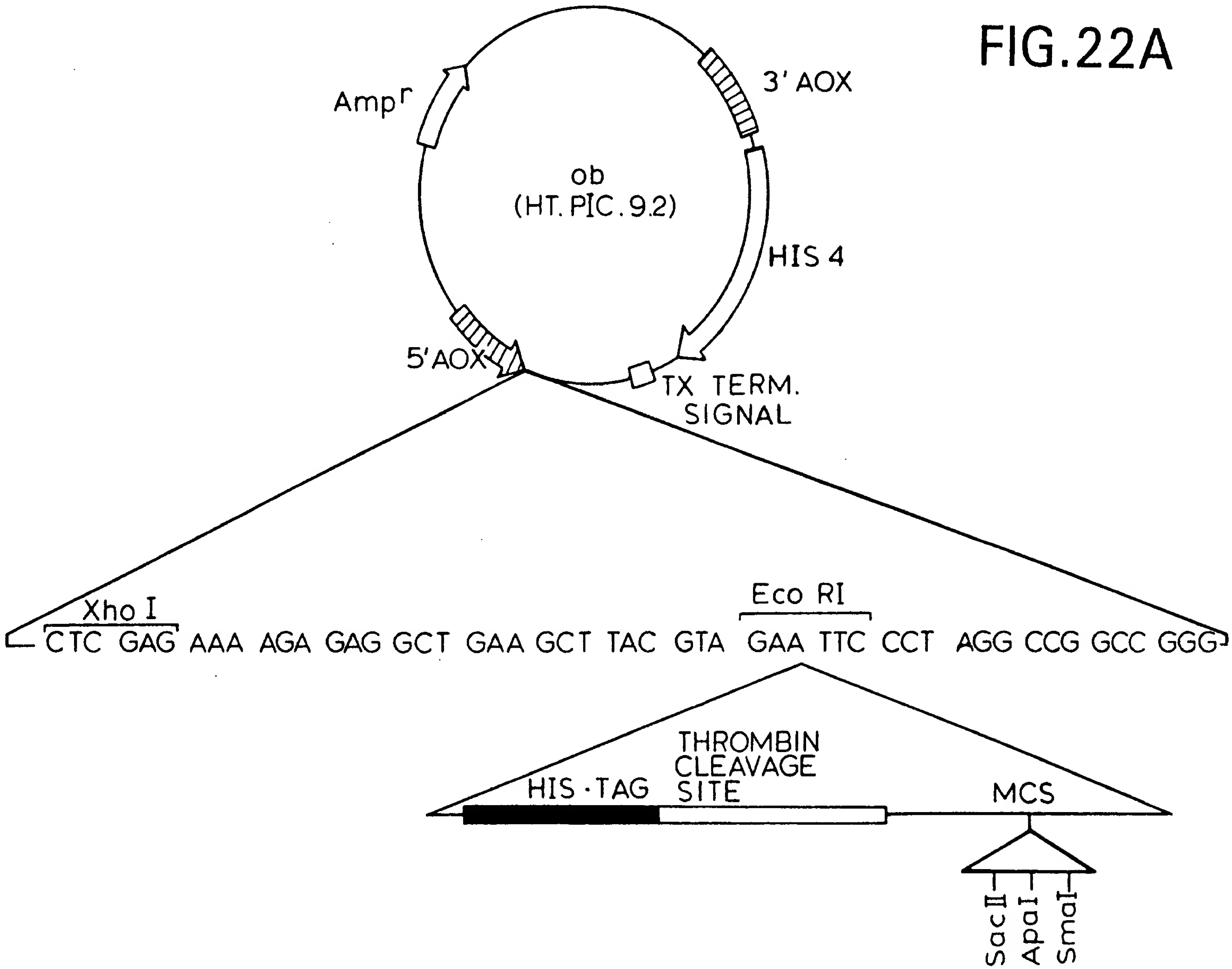


FIG.22A


Amp^r
ob
(HT. PIC. 9.2)
3' AOX
HIS 4
5'AOX
TX TERM.
SIGNAL
Xho I
Eco RI
CTC GAG AAA AGA GAG GCT GAA GCT TAC GTA GAA TTC CCT AGG CCG GCC GGG
HIS · TAG
THROMBIN
CLEAVAGE
SITE
MCS
SacII
ApaI
SmaI

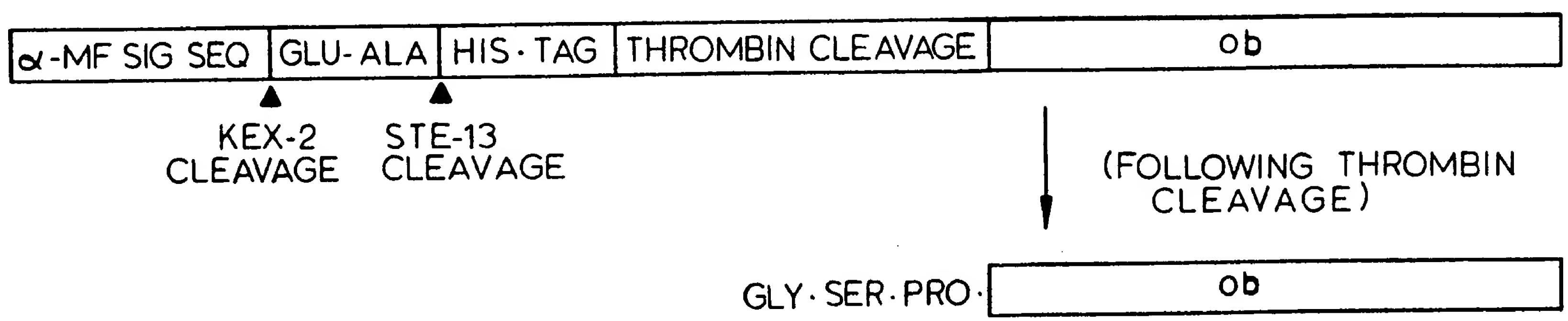

α-MF SIG SEQ
GLU-ALA
HIS·TAG
THROMBIN CLEAVAGE
ob
KEX-2 CLEAVAGE
STE-13 CLEAVAGE
(FOLLOWING THROMBIN CLEAVAGE)
GLY·SER·PRO·
ob

FIG.22B

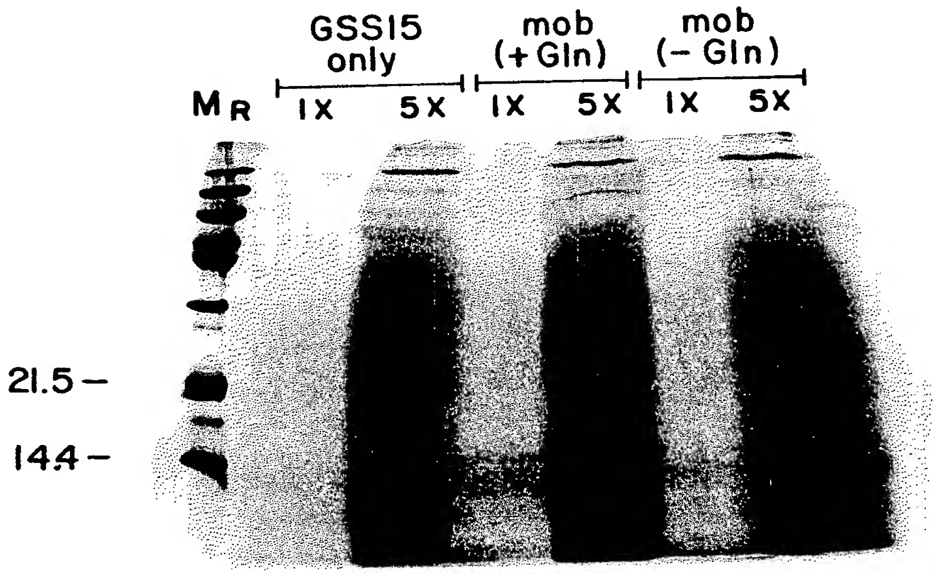


FIG.23A

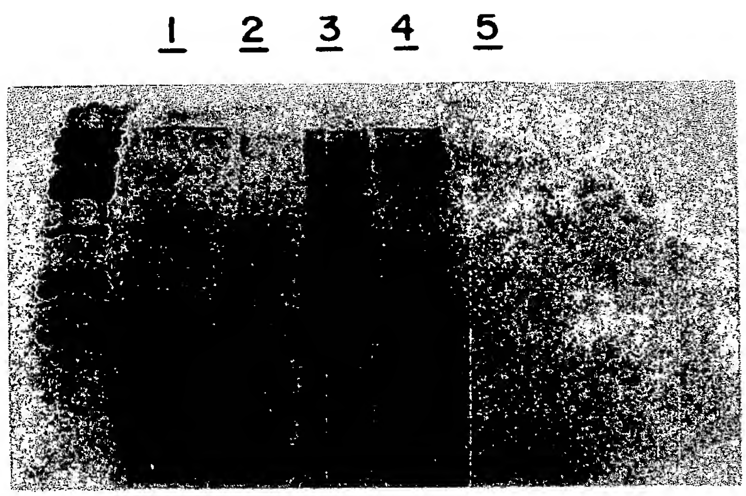


FIG.23B